```
================================================================
```
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=11; day=24; hr=10; min=49; sec=29; ms=158;
]
```
================================================================
```

```
****************************************************************
```
Reviewer Comments:

<160>     9


<170>     KopatentIn 1.71


The number provided for numeric identifier <160> must match the total
number of sequences in the file. There are 11 sequences in this sequence
listing but, 9 is given as the total in numeric identifier <160>, "<160>
9." Please make all necessary changes.


<210>   5
<211>   68
<212>   PRT
<213>   Artificial Sequence
<400>   5


For all sequences using "Artificial sequence", for numeric identifier
<213>, a mandatory feature is required to explain the source of the
genetic material. The feature consists of <220>, which remains blank,
and <223>, which states the source of the genetic material. To explain
the source, if the sequence is put together from several organisms,
please list those organisms. If the sequence is made in the laboratory,
please indicate that the sequence is synthesized. These errors appear in
other sequences in the sequence listing. Please make all necessary
changes.

* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Application No:　　10593413　　　　　Version No:　　　1.0

Input Set:

Output Set:

|  |  |
|---|---|
| **Started:** | 2008-10-28 16:16:48.335 |
| **Finished:** | 2008-10-28 16:16:52.980 |
| **Elapsed:** | 0 hr(s) 0 min(s) 4 sec(s) 645 ms |
| **Total Warnings:** | 9 |
| **Total Errors:** | 34 |
| **No. of SeqIDs Defined:** | 9 |
| **Actual SeqID Count:** | 11 |

| Error code | Error Description |
|---|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides  SEQID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides  SEQID (8) |
| E 300 | Invalid codon found   Gly SEQID  (8)  POS: 337 |
| E 300 | Invalid codon found   Gly SEQID  (8)  POS: 340 |
| E 300 | Invalid codon found   Ser SEQID  (8)  POS: 343 |
| E 300 | Invalid codon found   Ser SEQID  (8)  POS: 346 |
| E 300 | Invalid codon found   Ser SEQID  (8)  POS: 349 |
| E 300 | Invalid codon found   Gly SEQID  (8)  POS: 352 |
| E 300 | Invalid codon found   Thr SEQID  (8)  POS: 355 |
| E 300 | Invalid codon found   Val SEQID  (8)  POS: 358 |

**Input Set:**


**Output Set:**


|  |  |
|---|---|
| **Started:** | 2008-10-28 16:16:48.335 |
| **Finished:** | 2008-10-28 16:16:52.980 |
| **Elapsed:** | 0 hr(s) 0 min(s) 4 sec(s) 645 ms |
| **Total Warnings:** | 9 |
| **Total Errors:** | 34 |
| **No. of SeqIDs Defined:** | 9 |
| **Actual SeqID Count:** | 11 |

| Error code | Error Description |
|---|---|
| E 300 | Invalid codon found  Asn SEQID  (8)  POS: 361 |
| E 300 | Invalid codon found  Pro SEQID  (8)  POS: 364 |
| E 300 | Invalid codon found  Val SEQID  (8)  POS: 367 |
| E 300 | Invalid codon found  Pro SEQID  (8)  POS: 370 |
| E 300 | Invalid codon found  Thr SEQID  (8)  POS: 373 |
| E 300 | Invalid codon found  Thr SEQID  (8)  POS: 376 |
| E 300 | Invalid codon found  Ala SEQID  (8)  POS: 379 |
| E 300 | Invalid codon found  Ser SEQID  (8)  POS: 382 |
| W 213 | Artificial or Unknown found in <213>  in SEQ ID (9) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides  SEQID (9) |
| W 213 | Artificial or Unknown found in <213>  in SEQ ID (10) |
| E 323 | Invalid/missing amino acid numbering  SEQID (10)  POS (337) |
| E 323 | Invalid/missing amino acid numbering  SEQID (10)  POS (343) |
| E 323 | Invalid/missing amino acid numbering  SEQID (10)  POS (352) |
| E 323 | Invalid/missing amino acid numbering  SEQID (10)  POS (358) |
| E 323 | Invalid/missing amino acid numbering  SEQID (10)  POS (367) |
| E 323 | Invalid/missing amino acid numbering  SEQID (10)  POS (373) |
| W 213 | Artificial or Unknown found in <213>  in SEQ ID (11) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11) |

**Input Set:**

**Output Set:**

|  |  |
|---|---|
| **Started:** | 2008-10-28 16:16:48.335 |
| **Finished:** | 2008-10-28 16:16:52.980 |
| **Elapsed:** | 0 hr(s) 0 min(s) 4 sec(s) 645 ms |
| **Total Warnings:** | 9 |
| **Total Errors:** | 34 |
| **No. of SeqIDs Defined:** | 9 |
| **Actual SeqID Count:** | 11 |

| Error code | Error Description |
|---|---|
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides  SEQID (11) |
| E 252 | Calc# of Seq. differs from actual; 9 seqIds defined; count=11 |

<110>    SJ BIOMED INC.

<120>    Anti-obese immunogenic hybrid polypeptides and anti-obese vaccine composition comprising the same

<160>    9

<170>    KopatentIn 1.71

<210>    1
<211>    15
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    mimetic peptide for apolipoprotein B-100 epitope


<400>    1
Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe
 1               5                   10                  15


<210>    2
<211>    15
<212>    PRT
<213>    Artificial Sequence
<220>
<223>    mimetic peptide for apolipoprotein B-100 epitope


<400>    2
Arg Phe Arg Gly Leu Ile Ser Leu Ser Gln Val Tyr Leu Asp Pro
 1               5                   10                  15


<210>    3
<211>    15
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    mimetic peptide for apolipoprotein B-100 epitope


<400>    3
Ser Val Cys Gly Cys Pro Val Gly His His Asp Val Val Gly Leu
 1               5                   10                  15


<210>    4
<211>    204
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    DNA sequence for terameric mimetic peptide


<220>
<221>    CDS
<222>    (1)..(204)

<400>    4
gtc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca         48
Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala
 1               5                   10                  15

ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att         96
Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile
            20                  25                  30

gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg        144
Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
        35                  40                  45

att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat        192
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
    50                  55                  60

tgg att gca ttc                                                        204
Trp Ile Ala Phe
 65


<210>    5
<211>    68



<212>    PRT
<213>    Artificial Sequence
<400>    5
Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala
 1               5                   10                  15

Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile
            20                  25                  30

Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
        35                  40                  45

Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
    50                  55                  60

Trp Ile Ala Phe
 65


<210>    6

<211>    180
<212>    DNA
<213>    Hepatitis B virus

<220>
<221>    CDS
<222>    (1)..(177)
<223>    Hepatitis B virus preS2

<220>
<221>    terminator
<222>    (178)..(180)

<400>    6
atg cag tgg aac tcc acc aca ttc cac caa gct ctg cta gat ccc aga        48
Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg
 1               5                   10                  15

gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt tcc gga aca gta        96
Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
            20                  25                  30

aac cct gtt ccg act act gcc tca ccc ata tcg tca atc ttc tcg agg       144
Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
         35                  40                  45

act ggg gac cct gca ccg aac ctc gag cgg tca          taa        180
Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser
     50                  55


<210>    7
<211>    59
<212>    PRT
<213>    Hepatitis B virus

<400>    7
Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu Asp Pro Arg


 1               5                   10                  15
Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
            20                  25                  30

Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser Ile Phe Ser Arg
         35                  40                  45

Thr Gly Asp Pro Ala Pro Asn Leu Glu Arg Ser
     50                  55


<210>    8
<211>    444
<212>    DNA
<213>    Artificial Sequence

<220>

```
atg aga gga tcg cat cac cat cac cat cac gga tcc gat gat gat gac      48
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
1               5                   10                  15


aag atc gtc gac cgt aat gtt cct cct atc ttc aat gat gtt tat tgg      96
Lys Ile Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
                20                  25                  30


att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt tat     144
Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
        35                  40                  45


tgg att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat gtt     192
Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val
    50                  55                  60


tat tgg att gca ttc ctc gac cgt aat gtt cct cct atc ttc aat gat     240
Tyr Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp
65                  70                  75                  80


gtt tat tgg att gca ttc ctc gac atg cag tgg aac tcc acc aca ttc     288
Val Tyr Trp Ile Ala Phe Leu Asp Met Gln Trp Asn Ser Thr Thr Phe
                85                  90                  95


cac caa gct ctg cta gat ccc aga gtg agg ggc cta tat ttt cct gct     336
His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala
            100                 105                 110


ggt ggc tcc agt tcc gga aca gta aac cct gtt ccg act act gcc tca     384
Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser

            115                 120                 125


ccc ata tcg tca atc ttc tcg agg act ggg gac cct gca ccg aac ctc     432
Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Leu
    130                 135                 140


gag cgg tca taa                                                      444
Glu Arg Ser
145
```


<210> 9
<211> 147

<212> PRT
<213> Artificial Sequence

<400> 9
Met Arg Gly Ser His His His His His Gly Ser Asp Asp Asp Asp
1               5                   10                  15

Lys Ile Val Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp
            20                  25                  30

Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr
        35                  40                  45

Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp Val
    50                  55                  60

Tyr Trp Ile Ala Phe Leu Asp Arg Asn Val Pro Pro Ile Phe Asn Asp

65                  70                  75                  80
Val Tyr Trp Ile Ala Phe Leu Asp Met Gln Trp Asn Ser Thr Thr Phe
                85                  90                  95

His Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala
            100                 105                 110

Gly Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser
            115                 120                 125

Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Leu
    130                 135                 140

Glu Arg Ser
145


<210>       10
<211>       432
<212>       DNA
<213>       Artificial Sequence

<220>
<223>       DNA sequence for PTB14


<220>
<221>       CDS
<222>       (1)..(429)


<400>       10
atg aga gga tcg cat cac cat cac cat cac gga tcc gat gat gat gac      48
Met Arg Gly Ser His His His His His Gly Ser Asp Asp Asp Asp
1               5                   10                  15

aag atc gtc gac atg cag tgg aac tcc acc aca ttc cac caa gct ctg      96
Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu

```
cta gat ccc aga gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt          144
Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser
        35                      40                      45

tcc gga aca gta aac cct gtt ccg act act gcc tca ccc ata tcg tca          192
Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser
        50                      55                      60

atc ttc tcg aag act ggg gac cct gca ccg aac ctc gac cgt aat gtt          240
Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val
 65                     70                      75                      80

cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt aat             288
Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn
                85                      90                      95

gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac cgt             336
Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg
                100                     105                     110

aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc ctc gac             384
Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp
115                     120                     125

cgt aat gtt cct cct atc ttc aat gat gtt tat tgg att gca ttc     t           430
Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe
    130                     135                     140

aa                                                                  432
```

<210>   11
<211>   143
<212>   PRT
<213>   Artificial Sequence

<400>   11
```
Met Arg Gly Ser His His His His His His Gly Ser Asp Asp Asp Asp
 1               5                       10                      15

Lys Ile Val Asp Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu
                20                      25                      30

Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser
        35                      40                      45

Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Ser
        50                      55                      60

Ile Phe Ser Lys Thr Gly Asp Pro Ala Pro Asn Leu Asp Arg Asn Val

 65                     70                      75                      80

Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg Asn
```

85                      90                      95

Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp Arg
        100                     105                 110

Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe Leu Asp
        115                     120                 125

Arg Asn Val Pro Pro Ile Phe Asn Asp Val Tyr Trp Ile Ala Phe
    130                 135                 140